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Sequence 114, App
Sequence 109, App
Sequence 114, App
Sequence 114, App
Sequence 119, App
Sequence 114, App
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Sequence 126, App
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                                                                                                                           January 5, 2006, 20:53:35; Search time 46 Seconds (without alignments) 666.797 Million cell updates/sec
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Sequence 126,
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Sequence 102,
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: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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US-08-818-111-114
US-08-818-111-1109
US-09-072-596-1109
US-09-072-596-1109
US-10-103-002-109
US-10-103-002-109
US-10-103-002-109
US-10-103-002-109
US-10-084-843-114
US-09-073-010-126
US-09-073-010-126
US-09-287-849-26
US-09-287-849-12
US-09-072-596-107
US-09-072-596-107
US-09-072-596-107
US-09-072-596-107
US-09-818-111-101
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                                                                                                                                                                                                                                                                                                                                                                                572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
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Match Length
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Perfect score:
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Sequence 92, Application US/09050739
Patent No. 6641814
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSER, Peter Birk
APPLICANT: RASMUSER, Peter Birk
APPLICANT: RESENRANDS, 1da
APPLICANT: RESENRANDS, 1da
APPLICANT: PLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS
TITLE OF INVENTION: DETVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT PELLING DATE: 1998-03-30
CURRENT PELLING DATE: 1998-03-30
CURRENT PELLING DATE: 1997-11-10
EARLIER FILING DATE: 1997-11-10
EARLIER FILING DATE: 1997-10-10
EARLIER FILING DATE: 1997-10-10
EARLIER FILING DATE: 1997-10-10
EARLIER FILING DATE: 1997-10-10
EARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 92
LEARLIER FILING DATE: 1998-01-05
SEQ ID NO 92
LEARLIER PODERTOR NUMBER: 60/70,488
EARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
LEARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
LEARLIER FILING DATE: 1998-01-05
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Sequence 2, App
Sequence 109, A
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Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 371; Conservative 0; Mismatches 0; Indels 0;
US-08-818-111-106
US-09-056-556-111
US-09-072-596-106
US-09-072-596-106
US-10-193-002-106
US-10-193-002-106
US-08-444-623-2
US-08-444-623-2
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US-08-418-111-104
US-09-056-556-109
US-08-818-111-104
US-09-075-596-109
US-09-072-596-109
US-09-072-596-109
US-10-193-002-109
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US-09-050-739-92
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                             124 ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASQ
                                                     181 STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
                                                                                                                                                                                                244 GGNPADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLI
                                                                                                              STINPIFGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Campoe-Neto, Antonia
APPLICANT: Campoe-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210121.417C6
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; Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 2101
TELECOMMUNICATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 109:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 368 amino acids
amino acid
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CITY: Seattle
STATE: Washington
COUNTRY: USA
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US-08-818-111-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-818-111-109
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: TWARDYION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.0%; Score 1873; DB 2; Length 368; 99.7%; Pred. No. 6e-153; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION: NEFERRA
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 114, Application US/08818112
Patent No. 6290969
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INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
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STATE: Washington
COUNTRY: USA
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Best Local Similarity
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STRANDEDNESS: siz
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US-08-818-112-114
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TUBERCULOSIS
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SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT
                                                                            61 SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPE1AANHITQAVLT
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Compounds S.
APPLICANT: Compounds S.
APPLICANT: Compounds S.
APPLICANT: Compounds S.
APPLICANT: Mendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
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CURRENT APPLICATION DATA:
CURRENT APPLICATION UNDRER:
FILING DATE: 05-MAY-1998
CLASSIFICATION
ATTORNEY/AGENI INFORMATION:
ATTORNEY/AGENI INFORMATION:
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 109: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 368 amino acids
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STRANDEDNESS: single
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ZIP: 98104-7092
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US-09-072-596-109
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                                              SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT 123
                                                                                                                    ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPWASILDPGASQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 114, Application US/09056556

Sequence 114, Application US/09056556

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREE: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTY: USA.
                                                                 EKPVAPSVMPAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED
           1 MLWHAMPPEXNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVBLTARLNSLGBAWTGGG
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COMPUTER READABLE FORM:

MEDIUM TYBE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998
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ATTORNEY/AGENT INFORMATION:
NAME: MAKL, DAVIG J.
REGISTRATION NUMBER: 31,392
REPERROE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 367; Conserva
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STRANDEDNESS: sin
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US-09-056-556-114
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181 STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG 240
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                                                                                                                                                                                                                                Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         701 Fifth Avenue
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                                                                                                                                                                                                                                                                    Pred. No. 6e-153;
0; Mismatches
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                                                                                                                                                                                                                                                Score 1873;
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 109, Application US/10193002
Patent No. 6949246
GENERAL INFORMATION:
                 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
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                                                                                             : 368 amino acids
amino acid
                                                                                                                                                                                                                                                                    Best Local Similarity 99.7
Matches 367; Conservative
                                                                                                                                                  single
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                                                                                                                                                                         linear
                                                                                                                                             STRANDEDNESS:
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US-09-072-967-114
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US-10-193-002-109
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                                                                                                                                             4 MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
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                                                                                                  Gaps
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dangos-Neco, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Thomas S.
APPLICANT: Lodes, Michael J.
APPLICANT: Hondrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS SAND METHODS SAND METHODS SAND METHODS SAND METHODS SAND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS SAND METHODS SAND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS SAND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS SAND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUND AND DIAGNOSIS OF TUBERCULOSIS
COMPRESSOR SEND and BERRY LLP
                                                                                                  ;
0
                                                99.0%; Score 1873; DB 2; Length 368; 99.7%; Pred. No. 6e-153;
                                                                                                Indels
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                                                                                                0; Mismatches
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 114, Application US/09072967
Patent No. 6592877
                                                                                                Conservative
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                                                                      Best Local Similarity
Matches 367; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washingt
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION
US-09-072-596-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-072-967-114
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EXPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 ATNFEGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                 STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS
              Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1873; DB 2;
Pred. No. 6e-153;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFHONE: (206) 682-6031
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQUENCE DESCRIPTION: SEQ ID NO: 114: US-10-084-843-114
BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-073-009-126
; Sequence 126, Application US/09073009
Patent No. 6555653
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 368 amino acids
                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-60
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.0%;
Best Local Similarity 99.7%;
Matches 367; Conservative
 ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                     NAME: Maki, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alderson, Mark
                                  Seattle
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                   STREET: 6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASQ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STINPI FGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                         99.0%; Score 1873; DB 2; Length 368;
99.7%; Pred. No. 6e-153;
ive 0; Mismatches 1; Indels
                                                    PRIOR CARSAITCATION:

APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTONEY AGENT INFORMATION:
NAME: MAKi, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
          APPLICATION NUMBER: US/10/193,002
                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 109: US-10-193-002-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 114, Application US/10084843
Patent No. 6962710
GENERAL INFORMATION:
                           FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                         LENGTH: 368 amino acids
                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 99.7
Matches 367; Conservative
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GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
ITITLE OF INFORMATION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSES: SEED and BERRY
STREET: 6300 Coumbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 ALAAATPWVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQAVLTATN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 ------PLQQVTSLFSQVGG----TGGGNPADEEAAQMGLLGTSPLSNHP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 FGTPNFPTSISALLTDLQPYASXXYNTEGLPYFSIGMGNNFIQSAKTLGLIGSAAPAAVA 290
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30.6%; Pred. No. 2.7e-23;
tive 39; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,010
FILING DATE: 05-MAX-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 126:
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Best Local Similarity 30.6*
Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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          ; Patent No.
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                                                                                 TUBERCULOSIS AND ME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 MAEAVAPYVAWMSAAAAQAEQAATQARAAAAFEAAFAATVPPPLIAANRASLMQLISTN 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 AAVATAAGTAQSTLÍEMÍTGLÉN------ALÓSLISXLLQSSNGFLSWLWQIL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 FGTPNFPTSISALLTDLQPYASXXYNTEGLPYFSIGMGNNFIQSAKTLGLIGSAAPAAVA 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 VFGONTSAIAAAEAQYG-EMWAQDSAAMYAYAGSSASASASAVTPFSTPPQIANPTAQGTQA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 -----GASQST-TNPIFGMPSPGSSTPVGQLPPAATQTLGQ--LGEMSGPMQQLTQ-- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 -------PLQQVTSLFSQVGG----TGGGNPADEEAAQMGLLGTSPLSNHP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 LAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQL----1EK-----PVAPSVMP 313
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                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/073,009
FILING DATE: 05-MAY-1998
APPLICANT: Billon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Coumbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 210121.441C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 126: SEQUENCE CHARACTERISTICS: LENGTH: 400 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-MAY-1998 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: MAK1, David J. REGISTRATION NUMBER: 31,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.64
Matches 128; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                            98104
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341 GAAPLPVSTVSAAPEAAPGSLLGGLPLXGAGGAGAGPRYGFXPTVMARPPFXGIVAAA 398

; Sequence 126, Application US/09073010

RESULT 10 US-09-073-010-126

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SEQ ID NO 2
LENGTH: 729
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                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                      APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward H.
ITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
ITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 394;
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                                                                                                                                                                               TITLE OF INVENTION: INTERACTIONS OF PROTEINS FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR PELING DATE: 2000-10-28
PRIOR FILING DATE: 2000-02-01
PRIOR PILING DATE: 2000-02-01
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-13
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Sequence 205, Application US/09712363 Patent No. 6892139
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Matches 120; Conserv
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Sequence 2, Application US/09223040 Patent No. 6544522 GENERAL INFORMATION:

-09-223-040-2

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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT APPLICATION NUMBER: 1998-12-30
SUFMENT FILTE DATE: 1998-12-30
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFEKLEPMASILDPGASQSTTNPI-----FGMPSPGSSTPVGQL-----PPAATQTL 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTGG-TTPSSKLGGLWKTVSPHRSPIS 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AMPPELNTARLMAGAGPAPMLAAAAGWQTL----SAALDAQAVELTARLNSLGEAWTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 729;
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APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Dillon, Davin C.

APPLICANT: Alderson, Mark

APPLICANT: Corrix Corporation

APPLICANT: Corrix Corporation

TITLE OF INVENTION: Build Drotiens of Myc.

TITLE OF INVENTION: Total Uses

TITLE OF INVENTION: 1990-04-07

TITLE OF INVENTION NUMBER: US/09/287,849

CURRENT FILING DATE: 1990-04-07

PRIOR APPLICATION NUMBER: US 08/81P

PRIOR FILING DATE: 1997-03-17

PRIOR APPLICATION NUMBER: US 08/81P

PRIOR FILING DATE: 1997-03-17

PRIOR APPLICATION NUMBER: US 08/81P
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Matches 120; Conservative
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APPLICANT: Campos-Neto, Autonio
APPLICANT: Carac Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 NMVSWANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSSLGSSLGSS
381 NMVSWANNHMSSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSSLGSSLGSS 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVL 122
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PRIOR FILING DATE: 1997-03-13
PRIOR PELING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR PELING DATE: 1998-04-07
PRIOR PELING DATE: 1998-04-07
PRIOR PAPPLICATION NUMBER: US 09/056,556
PRIOR PAPPLICATION NUMBER: US 09/223,040
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
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Patent No. 6627198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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TUBERCULOSIS AND MA
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                                                                                                                 ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-09-287-849-26
                                                                                                                                                                                Length 596;
                                                                                                                                                                                                                                                                                                                                                                               123 TATNFFGINTIPIALTEMDYFIRMWOAALAMEVYQAETAVNT----
                                                                                                                                                                                                               Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Parent PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                               17.4%; Score 328.5; DB 2; 28.9%; Pred. No. 7.7e-20; tive 45; Mismatches 173;
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APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
AITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701 Fifth
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Patent No. 6555653
GENERAL INFORMATION:
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                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1998-12-30
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        NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
                                                                                                                                                                                                               Conservative
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STREET: 630.
TTW: Seattle
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                                                                                                                                                                                                               Matches 120;
                                                                  LENGTH: 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 QSTINPIFGMPSPGSSTPVGQLPP------AATQTLGQLGEMS--GPMQQLTQ 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AAATQAAGAGAVADAQATLAQLPPGILSDILSALAANADPLTSGLLGIASTLNPQVGSAQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 MPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAWTGGGSDKA 67
                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.2%; Score 326; DB 2; Length 423;
Best Local Similarity 30.4%; Pred. No. 7.9e-20;
Matches 121; Conservative 45; Mismatches 164; Indels 68; Gaps
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELECOMMULTOTION INFORMATION:
TELEPHONE: 206-622-4900
TELEPHONE: 206-682-6031
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: anino acid
TYPE: anino acid
TYPE: anino acid
TYPE: anino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-073-009-142
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Search completed: January 5, 2006, 21:19:28 Job time : 47 secs

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/ Search time 138 Seconds
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1181.228 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		_		_	_	Aaw32384 Mycobacte	Aaw32452 Mycobacte	Μγα	Σ	Σ	Σ.				_	Pr	_	Aaw73764 M. tuberc	Aau08225 Mycobacte	Abu34103 Protein e	Abm15864 Mycobacte	_	Abu34048 Protein e	Aag81154 Mycobacte	Adz36102 Mycobacte
SUMMARIES	£		AAW72929	AAY21946	AAB19844	ADG15733	AAW32384	AAW32452	AAW64338	AAW81705	AAY38992	AAY39135	ABU05362	ADG15750	ABU34364	AAB66451	ABU36905	AAW73654	AAW73764	AAU08225	ABU34103	ABM15864	ABU36014	ABU34048	AAG81154	ADZ36102
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	Query	MACCII	100.0	100.0	99.3	99.3	0.66	0.66	0.66	99.0	0.66	0.66	27.9	26.5	23.1	22.8	22.8	19.3	19.3	19.3	19.2	19.1	18.8	18.8	18.2	18.1
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~	Aae29708 Mycobacte	Aael7572 Mycobacte	Adf69753 Fusion pr	Ada26356 Mycobacte	Ada26368 Mycobacte	_	_	_	Adf69777 Fusion pr	Aau74599 Antigenic	Aao22142 Ra12-H9-3	Aae29709 Mycobacte	Aael7573 Mycobacte	Ada26374 Mycobacte	Ada26367 Mycobacte	Ada26366 Mycobacte	Ada26365 Mycobacte	Aae29731 Mycobacte	Ada26364 Mycobacte	Ada26370 M. bovis
ADA26373	AAE29708	AAE17572	ADF69753	ADA26356	ADA26368	AAY32070	AAE29710	AAE17574	ADF69777	AAU74599	AA022142	AAE29709	AAE17573	ADA26374	ADA26367	ADA26366	ADA26365	AAE29731	ADA26364	ADA26370
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ALIGNMENTS

Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen; New isolated mycobacteria polypeptides and nucleic acids - used for developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis. Rasmussen PB; Nielsen R, Rosenkrands I, Weldingh K, Florio W; Mycobacterium tuberculosis antigen RD1-ORF5 Claim 1; Page 200-202; 163pp; English. AAW72929 standard; protein; 371 AA 97DK-00000376. 97US-0044624P. 97DK-00001277. 98WO-DK000132. 98US-0070488P Mycobacterium tuberculosis. (STAT-) STATENS SERUM INST (first entry) WPI; 1998-542705/46. N-PSDB; AAV63939 02-APR-1997; 18-APR-1997; 10-NOV-1997; Andersen P, Oettinger T, 01-APR-1998; WO9844119-A1 21-JAN-1999 05-JAN-1998; 08-OCT-1998 infection AAW72929; RESULT 1 AAW72929

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

셤 ò 셤 δ 유 ઠે 셤 ઠે 셤 8 셤 ઠે 셤

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The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment (II) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M tuberculosis, and/or including a complex maino acid sequence from M: tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo confegration or post-translational processing; (3) a mucleic acid are useful as pharmaceutical, for diagnosis of and as antigens for that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceutical, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or brovious sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP10A. The polypeptides are also useful for diagnosing ongoing or cresponse in a mammal; use of for the induction of a strong immune crespitope of for diagnosis of TB in a mammal by performing a DTH type skin ceptic of for the preparation of an immunological composition; and cell epitope of for the preparation of an immunological composition; and cell epitope of for the preparation of an immunological composition; and cell epitope of for the preparation of an immunological composition; and cell epitope of for the preparation of an immunological composition; and cell epitope of for the preparation of an immunological composition; and cell and
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; Pred. No. 2.2e-131;
0; Mismatches 0;
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Example 2; Page 219-220; 265pp; English
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                              1 MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWT
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tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;
CFP7B; CFP19; CFP27; CFP30A; RDI-ORF; CFP10A; CFP16; CFP19; CFP23;
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                                                                                                                                                Length 371;
                                                                                                                                                                                                                                    Indels
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                                                                                                                                      Score 1892; DB 2;
Pred. No. 2.2e-131;
Mismatches 0;
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                                                                                              100.0%; Scc.
100.0%; Pre-
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                                                                                                                                                                                                                               Matches 371; Conservative
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N-PSDB; AAX81046.
                                                                                                                                                                                       Similarity
                                            Sequence 371 AA
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                                                                                                                                                                                                                                                                                                                                          The present sequence is that of the Mycobacterium tuberculosis MTBN3 protein. This is 1 of 8 proteins, i.e. WTBN1-8 (see AAB19842-49), encoded by 8 open reading frames (see AAA89035-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. WTBN1-8 represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these WTBN bolypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic (vaccine) methods, including genetic vaccination methods
                                                                                                                                                                                                                                                    Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Length 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.3%; Score 1878; DB 4; I
100.0%; Pred. No. 2.3e-130;
ive 0; Mismatches 0;
                                                                                                                                               (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 1; 35pp; English.
                                                                                        2000WO-US012257
                                                                                                                      99US-0132505P
   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 368; Conservative
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                                                                                                                                                                                                             2001-007153/01.
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                                                                                                                                                                                                                             N-PSDB; AAA89037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 368 AA;
                               WO200066157-A1
                                                                                                                      04-MAY-1999;
                                                                                        04-MAY-2000;
                                                            09-NOV-2000
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SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQAVLT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel diagnostic reagent comprising a peptide epitope from a protein encoded by the RD1 or RD2 regions of the Mycobacterium tuberculosis, M. bovis or M. africanum ganome. The diagnostic reagents comprised within the kit are selected so that they are able to differentiate between M. bovis, M. tuberculosis or M. africanum-infected mammals and mammals vaccinated against M. bovis, M. tuberculosis or M. africanum. The polypeptide or its variant or fragment is useful as a medicament provided that the polypeptide is not a MPT-64 polypeptide or a polypeptide encoded by the Rv1994 region of the M. polypeptide or a polypeptide or M. africanum genomes. The nucleic acid which encodes the polypeptide or the diagnostic reagents can be used as a vaccine, especially against Mycobacterium infections. This sequence corresponds to a protein used to derive the peptide epitopes used in the
                                                                                                                                                                antibacterial; antitubercular; tuberculostatic; vaccine;
diagnostic reagent; epitope; RD1 region; RD2 region;
Mycobacterium tuberculosis; Mycobacterium bovis; Mycobacterium africanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New diagnostic reagents comprising a peptide having an epitope from polypeptides Rv1986, Rv3878, Rv1983, Rv3873 or Rv3879 derived from RD1 and RD2 regions of Mycobacterium, useful as vaccines against
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                                                                                                              M tuberculosis Rv3873 protein for generating peptide epitopes
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Pred. No. 2.3e-130;
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100.0%; Pred. No. a...
'..a 0; Mismatches
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Matches 368; Conservative
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ADG15733;
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22-SEP-1995;
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Vedvick TH,
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                                                                                                                  360
EKPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED
                                                                       EKPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
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99.7%; Pred. No. 5.5e-130;
iive 0; Mismatches 1;
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DR;
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95US-00532136.
96US-00620280.
96US-00658800.
96US-00680573.
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Best Local Similarity 99.7
Matches 367; Conservative
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DWDEEDDW 368
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22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
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tuberculosis, also for
SDKALAAATPWVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT
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                                                                                        124 ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASQ
                                                                                                                                       STINDIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
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95US-00533634.
96US-00620874.
96US-00659683.
96US-00680574.
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                                                                                                                                                              SDKALAAATPWVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT 123
immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb37-FL The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
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                                                                                                                                       STINPIFGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
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                                                                                           Length 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tb37-FL.
                                                                                                               1;
                                                                                           Score 1873; DB 2;
Pred. No. 5.5e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis antigen Tb37-FL,
                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis; strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                AAW64338 standard; protein; 368
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97US-00818111.
                                                                                             99.0%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection;
                                                                                                              367; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                     368
                                                                                                                                                                                                                                                                                                                                     DWDEEDDW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                  DWDEEDDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Misc-difference
                                                                             Sequence 368 AA;
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09-NOV-1998
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                                                               prevention)
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Matches
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STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                           This polypeptide comprises Mycobacterium tuberculosis antigen Tb37-FL. I is encoded by genomic DNA isolated from a M. tuberculosis strain H37Rv genomic library using a probe from clone Tb38-1 (see AA44384). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AA44291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonuclectide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MIWHAMPPELNTARIMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARINSLGEAWTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                   New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
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Houghton
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Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.0%; Score 1873; DB 2;
99.7%; Pred. No. 5.5e-130;
ive 0; Mismatches 1;
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                                                                                                                                                                                                                                     Example 3; Page 143-144; 250pp; English.
Dillon DC, Ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368
  Skeiky YAW,
Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DWDEEDDW 371
                                                                             WPI; 1998-251292/22.
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AAY38992 standard; protein; 368

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                        Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method inducing protective immunity against tuberculosis (TB). This sequence be formulated into vaccines and/or pharmsceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STINPIFGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
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                                                                                                                                                                                                                                        Houghton R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1873; DB 2;
Pred. No. 5.5e-130;
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                                                                                                                                                                                                                                        Dillon DC, C
                                     Location/Qualifiers
                                                               /label= unknown
                                                                                                                                             97WO-US018293.
                                                                                                                                                                      96US-00730510.
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Best Local Similarity 99.7%;
Matches 367; Conservative
             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis of tuberculosis
                                                                                                                                                                                                                                                    Twardzik
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                                                                                                                                                                                                                                                                               WPI; 1998-261042/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 368 AA;
                                                   Misc-difference
                                                                                         WO9816646-A2
                                                                                                                                             07-OCT-1997;
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13-MAR-1997;
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                                                                                                                  23-APR-1998
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SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQAVLT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.
current
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel recombinant antigens and their encod mucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in biological sample by detecting antibodies which bind with the biological sample by detecting antibodies which bind with the tuberculosis, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as curvaccination strategies do not provide 100% immunity
                                                                                             diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                             tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 368;
                                                                                                                                                                                                                                                                                                 Houghton
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                                                                                                                                                                                                                                                                                                                                                           Σ̈́
                                                                      M. tuberculosis recombinant antigen protein Tb37-FL
                                                                                                                                                                                                                                                                                                Campos-Neto A, J, Hendrickson
                                                                                                                                                                                                                                                                                                                                                             polypeptide comprising antigenic portions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1873; DB 2;
Pred. No. 5.5e-130;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 177-179; 323pp; English.
                                                                                                                                                                                                                                                                                                siky YAW, Dillon DC, Са
Twardzik DR, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.0%;
                                                                                                                                                                                                            99WO-US003265
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98US-00072596
                                                                                                                                    Mycobacterium tuberculosis
                                              (first entry)
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Best Local Similarity 99.7
Matches 367; Conservative
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                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                             immunity
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                                                                                                                                                            W09942118-A2
                                                                                                                                                                                                                                    18-FEB-1998;
05-MAY-1998;
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                                                05-NOV-1999
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        GGNPADEBAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLI
                                                                                                                                                                                                                                                                                                                                                                              Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy.
                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis and M. leprae marker protein #13
                                                                                                                                                                                                                                                     ABU05362 standard; protein; 302 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2002; 2002WO-IB001973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-2001; 2001US-0270123P
                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis. Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 45.1
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method of the invention
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DWDEEDDW 368
                                                                                                                                        DWDEEDDW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INSP ) INST PASTEUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200274903-A2.
                                                                                                                                                                                                                                                                                                                   08-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-2002.
                                                                                                                                                                                                                                                                                      ABU05362;
           244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. M. tuberculosis Ag's. DNa encoding them, derived fusion proteins and polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis immune subjects. AAZ19295 to AAZ19460 and AAY39083 to AAX39225 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLWHAMPPEXIVTARLMAGAGPAPWLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPBIAANHITQAVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATWFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STINDIFGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STINPIEGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                  Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                         M. tuberculosis antigen Tb37-FL amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1873; DB 2;
Pred. No. 5.5e-130;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 132-133; 299pp; English.
                                                                             AAY39135 standard; protein; 368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.0%;
                                                                                                                                                                                                                                                                                                                                                                       99WO-US003268
                                                                                                                                                                                                                                                                                                                                                                                                       98US-00025197
98US-00072967
                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.0
Matches 367; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention
DWDEEDDW 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 368 AA;
                                                                                                                                                                                                                                                                                                         WO9942076-A2
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05-MAY-1998;
                                                                                                                                           05-NOV-1999
                                                                                                                                                                                                                                                                                                                                       26-AUG-1999
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361
                                                                                                           AAY39135;
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                                                                                                                                                                                                                                                                               This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from Mycobacterium tuberculosis and Mycobacterium tuberculosis and Mycobacterium tuberculosis and Mycobacterium leprae identified using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.
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Gaps

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Length 100 Indels

Score 502; DB 7; 1 Pred. No. 2.1e-29;

Query Match
26.5%; Score 502; DB
Best Local Similarity 100.0%; Pred. No. 2.1
Matches 100; Conservative 0; Mismatches

92

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151 9

1 ATAQAAAYTQAMATTPSLPEIAANHITQAVLTATNFFGINTIPIALTEMDYFIRMWNQAA ATAQAAAYTQAMATTPSLPEIAANHITQAVLTATNFFGINTIPIALTEMDYFIRMWNQAA

152 LAMEVYQAETAVNTLFEKLEPMASILDPGASOSTTNPIFG 191

19

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ABU34364 standard; protein; 445

RESULT 13 ABU34364 ID ABU

100

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258
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                                      OVGGTGGGNPAD----EEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSL 293
                                                                                                                                                                                                                                                                                                                                                         antibacterial; antitubercular; tuberculostatic; vaccine;
diagnostic reagent; epitope; RD1 region; RD2 region;
Mycobacterium tuberculosis; Mycobacterium bovis; Mycobacterium africanum.
39 IAAAKPMITWLQSA-----AEQTTTQAEAHRQAMASTPGMAVITENHITQAILATINF 91
                                                                                                                                                                        294 TRIPLMS--QLIEKPVAPS-----VMPAAAAGSSATGGAAPVGAGAMGQGAQSGGST 343
                                                                                                                                                                                    259 AWTPLWTGFQLIDKSIAPEPRQRVMLP-------PWAAGSPGHNAQDGGTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New diagnostic reagents comprising a peptide having an epitope from polypeptides Rv1986, Rv3878, Rv1983, Rv3873 or Rv3879 derived from RD1 and RD2 regions of Mycobacterium, useful as vaccines against
                          FGINTIPIALTEMDYFIRMWQAALAMEVYQAETAVNTLFEKLEPMASILDPGA-----
                                                                        --SQ--STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFS
                                                                                                                                              199 SIDSTGVYTSAQRGDTESAHRIGLFGASTLSSHPLVGITGTTTDTRLLCAESLPSASGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hewinson RG
                                                                                                                                                                                                                                                                                                                                  sequence fragment used to generate epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UKEN-) UK SEC FOR ENVIRONMENT FOOD & RURAL AFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 23; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gordon SV,
                                                                                                                                                                                                                                                          ADG15750 standard; protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-APR-2003; 2003WO-GB001815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002GB-00009723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vordermeier HM,
                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-903652/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003093307-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-2002;
27-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cockle PJ,
                                                                                                                                                                                                                                                                                                           26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-2003
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Mycobacterium bovis.

WO200277183-A2.

03-OCT-2002

Protein encoded by Prokaryotic essential gene #19891.

(first entry)

19-JUN-2003

ABU34364;

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antieense sequences given in the specification where expression of the 6213 antieense sequences given in the specification where expression of the expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cenceding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated contained by the nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the cartisense nucleic acid; (1) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular complification or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway to the proliferation or the biological captway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene compound activity; (12) determining the extent
                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 62288; 1766pp; English.
WPI; 2003-029926/02.
                                                                   N-PSDB; ACA38234
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The invention relates to a novel diagnostic reagent comprising a peptide epitope from a protein encoded by the RDI or RDZ regions of the diagnostic reagents ubscrollosis, M. bovis or M. africanum genome. The diagnostic reagents comprised within the kit are selected so that they are able to differentiate between M. bovis, M. tuberculosis or M. africanum-infected mammals and mammals vaccinated against M. bovis, M. tuberculosis or M. africanum. The polypeptide or its variant or fragment is useful as a medicament provided that the polypeptide is not a MPT-64 polypeptide or a polypeptide encoded by the Rv1984c region of the M. polypeptide or M. africanum genomes. The nucleic acid which encodes the polypeptide or M. africanum genomes. The nucleic acid which encodes the polypeptide or the diagnostic reagents can be used as a vaccine, especially against Mycobacterium infections. This sequence

method of the invention

Sequence 100 AA;

Zyskind JW; Xu HH;

罚袋

Ohlsen | Forsyth |

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

'n, Wang

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P.

21-MAR-2002; 2002WO-US009107

2002US-00072851

08-FEB-2002;

06-MAR-2002; 2002US-0362699P

(BLIT-) BLITRA PHARM INC. Zamudio C, Trawick JD, (INSP) INST PASTEUR

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12;
to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the identifying the antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational arung discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. arreus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIIGFIITLASNAQLLTE--FAINASYVAVGLLYAIAGVIDIVVEWVIGNLFGVVPLLGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; attenuated microorganism; Rv3018c;
signature tagged transposon mutant; mutant library;
mycobacterial infection; actinomycetales; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---T 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATGGAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 PSAELFVAAYVPYVAWLVQASADSAAAAGEHEAAAAGYVCALAEMPTLPELAANHLTHAV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPWASILDPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLLGA------LAAAVVPGVAG-----LAGVAGLAAVPAVGAAAGAPAALVGSVA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                       GGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAV 121
                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                   73
                                                                                                                                                                                                                                                                                                                                                                                       14 IPVWLASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSAVVAAVGAGVWQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 QTLGQLGEMSGPMQQLTQPLQQVTSLFSQVG---GTGGGNPADEEAAQMGLLGTSPLSNH
                                                                                                                                                                                                                                                                                                                                                            3 TMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGE-AWTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 ANEASNAVAAATITPFPWHEIVQFLEETFAAYDQYLSALLSELPAVAWVWFQLFVDILGF
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                       Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Mycobacterium tuberculosis Rv3018c gene.
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASQ----STINPI-----FGMPSPGSSTPVGQLPPAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVGAGAMGQGAQSGGSTRPGLVAPAP----LAQER 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVSGGVVSPQARLVSAVEP---APASTSVSVLASDR 387
                                                                                                                                                                                                                                                                                                                          45; Mismatches 155;
                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                       23.1%; Score 436.5; DB 6
33.6%; Pred. No. 8.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB66451 standard; protein; 434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-2000; 2000WO-IB000950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 33.6%
Matches 133; Conservative
                                                                                                                                                                                                                                                      Sequence 445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200102555-A1.
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08-JUL-1999;
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The present sequence is given in a specification relating to a method for screening a library of mutants. The method comprises constructing a library with insertions in genes and/or regulatory regions of the organisms of interest, where the insertion contains a teg and/or a corganisms of interest, where the insertion contains a teg and/or a cransposon associated with a tag. The mutants are identified by transposon associated with a tag. The mutants are identified by creating an individual suffering from a mycobacterial infection, suspected of being infected with a Mycobacterium, or having been exposed to an infectious Mycobacterium. It is also useful for identifying and isolating mutants of actinomycetales and for identifying compounds that have antibiotic activity. The method is used to identify mutants of microorganisms, preferably an actinomycetales, such as M. tuberculosis, C. microorganisms, mavium, M. intracellulaire and M.

The bovis, M. leprae, M. avium, M. intracellulaire and M.

The paratuberculosis, that is unable to grow under specific conditions. It is especially useful for identifying loci involved in pathogenicity. It is caseful in constructing vaccines. The method can be used to screen conditions or different strains of the same organism. The present procein is encoded by a gene which is disrupted by the insertion of the IS 1096 transposon to produce an attenuated mutant of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVLTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 OGPSAELFVAAYVPYVAWLVQASADSAAAGEHEAAAAGYVCALAEMPTLPELAANHLTH 120
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                                                                                                                                                                       Screening a mutant library for mutants unable to grow under specific conditions and for identifying loci involved in pathogenicity, comprises using signature tagged transposon mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 VAPVSGGVVSPQARLVSAVEP---APASTSVSVLASDR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
22.8%; Score 430.5; DB 4;
Best Local Similarity 33.2%; Pred. No. 2.4e-23;
Matches 132; Conservative 45; Mismatches 158;
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                                                                                                                                                                                                                                                                       Example 8; Fig 20A; 159pp; English
                                                                Camacho L;
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                                                                Guilhot C,
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                                                                                                                                   N-PSDB; AAF31607
                                                                Gicquel B,
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the invention trained to an isobate and act to compare any properties of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promiter proliferation of a cell. Also included are:

(1) a vector comprising a promiter proliferation of a cell. Also included are:

(1) a vector comprising a promiter proliferation of the nucleic acid.

(2) a host cell containing the vector; (3) an isolated of nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the captised for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits proliferation of an organism and approximated for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits the extent of product is overexpressed or underexpressed; (12) determining the extent of product is overexpressed or underexpressed; (12) determining the extent of product is overexpressed or underexpressed; (12) determining the extent of compound setzains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for groliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. promity discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. the target prokaryotic essential genes. Note: The sequence data for this specification, or the printed specification, but was obtained to the print of the printed specification, the printed specification, the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW;
Xu HH;
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Forsyth RA,
                                                                                                        Protein encoded by Prokaryotic essential gene #22432
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Yamamoto R,
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2002; 2002US-00072851
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                                                                                                                                                                                                                                                                                                                         21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                            Mycobacterium tuberculosis
                                                             (first entry)
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Trawick JD,
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N-PSDB; ACA40775.
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                                                             19-JUN-2003
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Wall
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6; Length 434; Score 430.5; DB 6 Pred. No. 2.4e-23; 22.8%; 33.2%; Query Match Best Local Similarity

12; 178 180 PGANEASNAVAAATITPFFPWHEIVQFLEETFAAYDQYLSALLSELPAVAWVWFQLFVDIL 239 264 297 324 298 GGPLLGA-----LAAAVVPGVAG-----LAGVAGLAALPAVGAAAGAPAALVGS 341 59 9 240 GFNIIGFIITLASNAQLLTE--FAINASYVAVGLLYAIAGVIDIVVEWVIGNLFGVVPLL 1 MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGE-AW 60 TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ 120 AVLTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPMASILD 209 -TQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVG---GTGGGNPADEEAAQMGLLGTSPLS 265 NHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATGG 1 MTAPVWLASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSVVVAAVGAGVW PGASQ----STINPI-----FGMPSPGSSIPVGOLPPAA-----63; Gaps Indels 325 AAPVGAGAMGQGAQSGGSTRPGLVAPAP----LAQER 357 342 VAPVSGGVVSPQARLVSAVEP---APASTSVSVLASDR 376 45; Mismatches 158; Matches 132; Conservative 179 엄 ö 셤 ò 셤 à g à 셤 g ò à à

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STRAIN=CDC 1551 / Obhkosh;
MEDLINE=220494; PubMed=12218036;
MEDLINE=22204184.19.5479-5490.2002;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hetcky R.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.E., Khouri H.M. Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Praser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corymebacterineae, Mycobacteriaceae, Mycobacterium, Mycobacterium tuberculosis complex.
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Interpropriate PPE, 1.
SEQUENCE 371 AA; 37686 MW; CC25F5865131C79B CRC64;
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99.7%; Pred. No. 4.3e-98;
iive 0; Mismatches 1;
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EMBL; AE000516; AAK48355.1; -; Genomic_DNA.
TIGR; MT3987; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPE family protein.
OrderedLocusNames=MT3987;
Mycobacterium tuberculosis.
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Q7D4P4;
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MEDLINE-22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
MEDLINE-2709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
MEDLINE-2709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
Paryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
InterPro; IPR000030; Microbac_PPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium,
Mycobacterium tuberculosis complex.
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                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0T-2004 (TrEMBLrel. 26, Last annotation update)
PPL FAMILY PROFISIN.
NG-EPPE68, OrderedLocusNames-WD3903;
M. Cobacterium bovis.
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SEQUENCE 368 AA
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241
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MEDLINE-9829597; PubMed=9634230; DOI=10.1038/31159;
MEDLINE-98295987; PubMed=9634230; DOI=10.1038/31159;
MEDLINE-98295987; PubMed=9634230; DOI=10.1038/31159;
MEDLINE-98295987; PubMed=96.34230; DOI=10.1038/31159;
Harris D.E., Gordon S.V., Elglmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Kroph A., McLean J., Moule S.,
Murphy L.D., Oliver S., Seeger K., Skelton S., Squares S., Squares S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Mature 393:537-544(1998).
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                                                                                                                                                                                  Name=PPE68; OrderedLocusNames=Rv3873; Mycobacterium tubercullosis.
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales; Corynebacterines; Mycobacteriaces; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 AA; 37330 MW; D78F44095F658CA2 CRC64;
                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
PPE FAMILY PROTEIN
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Tuberculist; RV3873; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PP00823; PPE; 1.
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MYCTU PRELIMINARY;
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MEDLINE-17,
MEDLINE-17,
MEDLINE-17,
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Cole S.T., Eiglmeier K., Parkhill J., Churcher C.M., Harris D.E.,
Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E.,
Mungall K.L., Basham D., Brown D., Chillingworth T., Comnor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
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                                                                                                                                                                                                                                                                                         Biglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.; "Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae."; Mol. Microbiol. 7:197-206(1993).
                                                                                                                                                  Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
Eiglmeier K., Garnier T., De Rossi E., Fsihi H., Cole S.T.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 302 AA; 32135 MW; EDAC4CCOAF3BF3D0 CRC64;
                                                                01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annocation update)
Hypothetical protein MLCB678.14c (PPE-family protein)
Name-MLCB628.14c; OrderedLocusNames=ML0051;
                                                                                                                                                                                          Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL: 71.967; CAR75201.1; -; Genomic DNA.
EMBL: ALS81917; CAC29559.1; -; Genomic_DNA.
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InterPro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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                                               (TrEMBLrel. 05,
O33085_MYCLE PRELIMINARY;
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Leproma, ML0051; -.
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Matches 134; Conserv
                                                                                                                                                                                                              NCBI_TaxID=1769;
                                               01-JAN-1998
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----QPLQQVTSL----PSQVG---GTGGGNPADBEAAQM-------GLLGTSP 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 TGGGSDKALAAATPWVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELPAAWHITQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 AVLTATNPFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGASQSTTNPIFGMPSPGSSTPVGQLP---PAATQTLGQLGEM-----SGPMQQLT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 GLVNFEPWLVLTGMIDMFFATVGFALGVFVLVPLLEFAVVLELAILSIGWIISNIFGAIP 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGE-AW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                MEDINESTRONGY; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating IL., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

EMBL; BX248344; CAD95734.1; -; Genomic_DNA.

InterPro; IPR000030; Microbac_PPE.
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                                                                                                                                                                                        Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435 AA; 42878 MW; 62A5615EB0D0DEED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 GGAAPVGAGAMGQGAQSGGSTRPGLVAPAP----LAQER 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 GSVAPVSGGVVSPQARLVSAVEP---APASTSVSVLASDR 377
                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.5%; Score 445; DB 2; 34.0%; Pred. No. 3.6e-17;
       435 AA
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                                                                                                                                           Name=PPE47; OrderedLocusNames=Mb3047c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                      Mycobacterium tuberculosis complex
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QTIXF6_MYCBO PRELIMINARY;
Q7IXF6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                      Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                               01-MAR-2004 (Tremble PPE FAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome SEQUENCE 435 AA
                                                                                                                                                                                                                                                                    NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                           STRAIN=AF2122/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPE47 MYCTU
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PGANEASNAVAAATITP---FPFGELAKFLEMAAQAFTEVGELIMKSAEAWAVGFVELIT 236
                                                                                                                                                                 237 GLVNFEPWLVLTGMIDMFPATVGPALGVFVLVPLLEFAVVLELAILSIGWIISNIFGAIP 296
                                                                                                                                                                                                                         LSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSAT 322
                                                                                                                                                                                                                                                                                  297 VIGGPLICA------LAAAVVPGVAG-----LAGVAGLAALPAVGAAAGAPAALV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 LTATNFFGINTIPIALTEMDYFIRMWNQAALAMBVYQAET-AVNTLFEKLEPMASILDPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 NIIGFIITLASNAQLLTE--FAINASYVAVGLLYALAGVIDIVVEWVIGNLFGVVPLLGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATGGAA 326
PGASQSTTNPI FGMPSPGSSTPVGQLP---PAATQTLGQLGEM-----SGPMQQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TPVWLASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSAVVAAVGAGVWQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 ANEASNAVAAATITPFPWHEIVQFLEETFAAYDQYLSALLSELPAVAWWFQLFVDILGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 QTLGQLGEMSGPMQQLTQPLQQVTSLFSQVG---GTGGGNPADBEAAQMGLLGTSPLSNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garnier T., Bigimeier K., Camus J.-C., Medina N., Mansoor H., Proor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Arkin R., Dogget U., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

EMBL, BX248344, CAD96730.1; -; Genomic_DNA.

Interpro; IPR000030; Microbac_PPR.

EMBL, PR0833; PPE; 1.

Complete proteome.

SEQUENCE 437 AA; 43383 MM; 2B295898155009D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Mismatches 155; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                              ----QPLQQVTSL----FSQVG---GTGGGNPADEEAAQM-
                                                                                                                                                                                                                                                                                                                                              GGAAPVGAGAMGQGAQSGGSTRPGLVAPAP----LAQER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=PPE46; OrderedLocusNames=Mb3043c;
Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7TXF8 MYCBO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 133; Conservative
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179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVLTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                                                                         MEDLINE=9935987; PubMed=9634230; DOI=10.1038/31159;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares
Sulscon J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTAPUWLASPPEVHSALLSAGPGPGSLOAAAAGWSALSAEYAAVAQELSVVVAAVGAGVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CDC 1551 / Oshkosh;
MEDLINE-22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Polischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Eraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toa
Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 1; Length 435; 6.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.3%; Score 440; DB 1; Length 43: Best Local Similarity 33.5%; Pred. No. 6.9e-17; Matches 134; Conservative 51; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 184:5479-5490(2002).
-!- SIMIGARITY: Belongs to the mycobacterial PPB family.
-!- CAUTION: Ref.1 Bequence differs from that shown due frameshift in position 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
299 G -> A (in Ref. 2).
320 Logy -> VIGL (in Ref. 2).
326 L -> V (in Ref. 2).
42877 MW; 3B157643EAAR484A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BX842581; CAES5541.1; ALT FRAME; Genomic_DNA.
EMBL; BX842581; CAES5542.1; ALT_FRAME; Genomic_DNA.
EMBL; AE000516; AAK47435.1; -; Genomic_DNA.
              Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuberculist; Rv3021c; -. Tuberculist; Rv3022c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               laboratory strains.";
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SO WERE REPORTED TO THE PROPERTY OF THE PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVLTATIVERGINTIPIALTEMDYFIRWWNQAALAMEVYQABTAVNTLFEKLEPWASILDP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AALQATNFFGINTIPIAVNEADY-ARMWVQAATTWTTYQ---AVSTAAVAATPQ-TMPAP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVTSLFSQVGGTGGGNPADEEAAQMGLLGTSPLSNHPLAGG-----SGPSAGAGLLRAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 AVTSIGAAAGAAGG-----LVGLAGLA--SPGPLPTGAEMVPVTAPPPGATPAPTA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLLGA------LAAAVVPGVAG-----LAGVAGLAAVPAVGAAAGAPAALVGSVA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 ANLAGTPAKLAQIFSNPSVLFSWPTLLWVLDFIAGRIFDILVTLKFLLEQPLLYVVGLGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017240; AASO6275.1; -; Genomic_DNA.
InterPro; IFR000030; Microbac_PPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 AA; 52170 MW; BAC863B26F9CCF62 CRC64;
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.9%; Score 432.5; DB 2;
llarity 32.6%; Pred. No. 2.2e-16;
Conservative 41; Mismatches 155;
                                                                 PVGAGAMGQGAQSGGSTRPGLVAPAP----LAQER 357
                                                                                                                   347 PVSGGVVSPQARLVSAVEP---APASTSVSVLASDR
                                                                                                                                                                                                                                                                    518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 AA
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                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                              Q73TJ3 MYCPA PRELIMINARY;
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es 143; Conserv
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P31500; 053265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=k10;
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Matches
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                                                                                                                                                                                                                                         셤
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CDC 1551
MEDLINE-22206494; PubMed-12218036;
MEDLINE-22206494; PubMed-12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Polsischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Feterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Eraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome comparison of Mycobacterium tuberculosis clinical and
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SUSTAIRS OF SU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Isolate 50410;
Backi A.H., Dale J.W.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the mycobacterial PPB family.
-!- CAUTION: In strain Oshkosh the gene for this protein is
interrupted in position 307 by an IS6110 element.
-!- CAUTION: Was originally (Ref.3) thought to be a dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                            Macteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterinea; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteome; Hypothetical protein.
434 AA; 43029 MW; 41D673C4BD389DD6 CRC64;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical PPE-family protein PPE46.
Name-ppe46; OrderedLocusNames=Rv3018c, MT3098/MT3101;
ORFNames=MTV012.32c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BX842581; CAES5538.1; -; Genomic_DNA.
EMBL; AE000516; AAK47427.1; ALT_SEQ; Genomic_DNA.
EMBL; AE000516; AAK47430.1; ALT_SEQ; Genomic_DNA.
EMBL; X50271; CAA41961.1; ALT_FRAME; Genomic_DNA.
PIX; R70857; E70857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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Pfam; PF00823; PPE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
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DB 1; Length 434;

22.8%; Score 430.5;

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120 AVLTATIVEFGINTIPIALTEMDYFIRMWNOAALAMEVYQAET-AVNTLFEKLEPMASILD 178
                                                          ----LTOPLOOVTS-----LFSQVGGTGGGNPADEEAAQMGLLGTSPLSNH 266
                                                                                                                                                                                                                                                                                      ----PTWGMILSSPFL-L 279
                                                                                                                                                                                                                                                                                                                                      PLAGGSGPSAGAGL --- LRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATG 323
                                                                                                                                                                                                                                                                                                                                                                                      280 PAGLGLGLALAIAFLPIVLAPAVIPPAS-----TPLAAAAV---AAGSVWPAV---SMAVT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
STRAIN=H37Rv;
MIRDLINE=8829587; PubMed=9634230; DOI=10.1038/31159;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Tolonor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skeltwell M.A., Rajandream M.A.,
Sulston J.E., Taylor K., Whitchead S., Barrell B.G.,
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                PGGGAAST-----VGAVNPWQWLLALLQQLWNAYTGFYGWMLQLIWQFLQDPIGNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21206494; PubMed=12218036; MEDLINE=21206494; PubMed=12218036; DOI=10.1128/JB.184.19.5479-5490.2002; Peterson J.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDEDDW 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 GAGTAGAATPAAGAAPSAGAAPAPAAPATASFAYAVGGSGDW 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                      PPE family protein.
Name=PPE4; OrderedLocusNames=MT0299, Rv0286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000516; AAK44523.1; -; Genomic_DNA
EMBL; BX842573; CAE55266.1; -; Genomic_DNA
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Tuberculist; Rv0286; -.
InterPro; IPR000030; Microbac_PPE.
Emp. PF00823; PPE; 1.
Complete proteome.
SEQUENCE 513 AA; 51787 MW; E8F
                                                                                                                             PGASQSTTNPIFGMPSPGSSTP-
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Nature 393:537-544 (1998).
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Q7DA35; Q6MX52;
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                                                                                                                                                                                TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ 119
                                                                                                                                                                                                                AVLTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                         180 PGANEASNAVAAATITPFPWHEIVQFLEETFAAYDQYLSALLSELPAVAWVWFQLFVDIL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFNIIGFIITLASNAQLLTE--FAINASYVAVGLLYAIAGVIDIVVEWVIGNLFGVVPLL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 GGPLLGA------LAAAVVPGVAG------LAGVAGLAALPAVGAAAGAPAALVGS 341
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                                                                                                                     1 MTAPVWLASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSVVVAAVGAGVW
                                                                                                                                                                                                                                                                                                                                                                                         PGASQ----STTNPI------FGMPSPGSSTPVGQLPPAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 -TQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVG---GTGGGNPADEEAAQMGLLGTSPLS
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                             Gaps
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MEDLINE-22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Colls S.T., Gordon S.V., Hewinson R.G.;
Froc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
EMBL; BX248335; CAD93158.1; -; Genomic_DNA.
                          63;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PPE FAMILY PROTEIN.
Name=PPE4, Order-GLOCUSNAmes=Mb0294;
Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacterldae; Actinomycetales;
                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 VAPVSGGVVSPQARLVSAVEP---APASTSVSVLASDR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae; Mycobacteriaceae; Mycobacterium;
; Pred. No. 2.3e-16;
45; Mismatches 158;
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33.2%;
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Q7U2C9;
                          Matches 132; Conservative
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Complete proteome.
SEQUENCE 513 AA; 517
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Best Local Similarity
Similarity
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60 TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPRIAANHITQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AALVATNIFIGINTIPIALNEADY-ARMWOAATTMSTYQ---TVSTSTLAAAPRISSAAPA 176
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                                                                                                                                                                                                                                                                       NHPLAGGSGPSAGAGLIRAESLPGAGGSLTRTPLMSQLIBKPVAPSVMPAAAA--GSSAT 322
127 GALVATNFFGINTIPIAVNEADY-ARMWVQAAGTWATYQAVSTAAVAAVPQPDPAPSILK 185
                                                                                     |: | :: | |: | |: | STAAHDHDHGFDSPINQFVAQILRLFGIDWDPVEGTLNGLPYEAYTSPA 245
                                                                                                                                                              ----DEBAAQM-GLLGTSP-LS 264
                                                                                                                                                                                                                  246 DPLWWVVRALELFSDFQQFGALLQENPAARQFITELVLLDWPTHLAQLASWLPTQPQLL 305
                                                                                                                                                                                                                                                                                                          177 IVKSEDSSAGDTGDSSGGGGFFGDLLSAWENFVMNLMDQLFGVDSP------PDLAS
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22.4%; Score 423.5; DB 2; Length 504;
Best Local Similarity 32.9%; Pred. No. 6.8e-16;
Matches 138; Conservative 39; Mismatches 140; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kapur V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corymebacterineae, Mycobacteriaceae, Mycobacterium, Mycobacterium avium complex (MAC).
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AS017240; AAS06287.1; -; Genomic_DNA.
InterPro; IFR000030; Microbac_PPE.
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SEQUENCE 504 AA; 49761 MW; 4DD3E220EB495932 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                      GGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLA 354
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OrderedLocusNames=MAP373;
Mycobacterium paratuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 AVLTATNPEGINTIPIALTENDYPIRMWQAALAMBVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 KIIIAFLTNPIQALITYGPLLFALGYQIFFNLVGW------PTWGMILSSPFL-L 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                            TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPBIAANHITQ 119
                                                                                                                                                                                                                                                                                                                                                                                                       121 TVLVATNPFGINTIPITINEADY-VRMMIQAAAVMGLYQAASGAALASAPRTVPAPTVMN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LIQPLQQVTS-----LFSQVGCTGGGNPADEEAAQMGLLGTSPLSNH 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 PLAGGSGPSAGAGL---LRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATG 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 PGGGAAST-----VGAVNPWQWLLALLQQLWNAYTGFYGWMLQLIWQFLQDPIGNSI
                                                                                                                                                   MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAW
                                                                                                                                                                                                      1 MAAPIWMASPPEVHSALLSNGPGPGSLVAAATAWSQLSAEYASTAABLSGLLGAVPGWAW
                                                                                                Gaps
                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGASQSTINPIFGMPSPGSSTP-----VGQLPPAATQTLGQLGEMSGPMQQ-
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                                       Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017239; AAS06640.1; -; Genomic_DNA.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Complere proteome; Hypothetical protein.
SEQUENCE 531 AA; 53742 MW; B392FEI19582DC8C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                          ; Score 430.5; DB 2;
; Pred. No. 2.8e-16;
44; Mismatches 155;
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                                             22.8%;
33.3%;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Hypothetical protein.
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Best Local Similarity 34.9%
Matches 137; Conservative
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                                                                                                134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q73U78_MYCPA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVLTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQA--ETAVNTLFEKLEPMASIL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 DPGAS------PPAATQTLG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 QLGEMSGPMQQLTQPLQQVTSL-FSQVGGTGGGNPADEEAAQMGLLGTSPLSNHPLAGGS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAPVLPGVAAAPSGGGAAAVLAPGPGASAATVSPAPAPAGMPATAPAPAPGPPTPPPATGV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 GPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPV-APSVMPAAA-----AGSSA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWOTLSAALDAQAVELTARLNSL-GEAW
                                                                                                                                                                                                                                                                                                                                                                                                                      60; Gaps
                                                                                                                                                                                                                                                                                Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017230, AA503461.1; -; Genomic_DNA.
InterPro; IPR000030; Microbac_PPE.
Pfan, PF00823; PPE; 1.
CComplete proteome.
SEQUENCE 488 AA, 48598 MW, C2FD0PB977DE334B CRC64;
                                                                                         0741E7;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypochetical protein.
07-deredLocusNames=MAP1144;
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriace; Mycobacterium;
Mycobacterium avium complex (MAC).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
07-GreedLocusNames=MAP1813c;
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | | | | : | | | : | | | : | | BGFSAPYAVGPPGLGAGGNLSAGTRAGQTSPDFATAAAPAAADRRE 393
                                                                                                                                                                                                                                                                                                                                                                                           Length 488;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.1%; Score 419; DB 2; Length 480
Best Local Similarity 32.8%; Pred. No. 1.2e-15;
Matches 133; Conservative 45; Mismatches 168; Indels
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Q73XZ0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 APGAEAGAATAAAVQSAAAAPATDSGSNLNHADTSSIQQQASTAAQSYPSWQDQLTAWLK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 QVTSLFS---QVGGTGGGNP----ADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 RAESLPGAGGSLTRT----PLMSQLIEKPVAPSVMPAAAAGSSATGGAAPVGAGAMGQG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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WUCLEOTIDE SEQUENCE.
STRAIN=k10;
Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databasee.
EMBL, AE017231, AAS04130.1; -', Genomic_DNA.
InterPro; IPR000030; Microbac_PPB.
Complete Proteome.
SEQUENCE 550 AA; 54593 MW; E974C5075A847ECE CRC64;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).
                                                                                                                                                                                                                                                                                                                       21.6%; Score 408.5; DB 2; 32.0%; Pred. No. 5.2e-15; iive 48; Mismatches 162;
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datches 121; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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January 5, 2006, 16:44:30; Search time 40 Seconds (without alignments) 892.410 Million cell updates/sec Run on:

US-09-872-505A-6 1892 1 MITMLWHAMPPELNTARLMA......PLAQEREEDDEDDWDEEDDW 371 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		ical	PPE	PPE	PPE	PPE		PPE	PPE	PPE		PPE	PPE	PPE	PPB	PPE	PPE	PPE	ical	PPE	PPE		PPE	probable PPE prote	y pr	probable PPB prote	cal	PPE	probable PPE prote
	ΙD	G70802	T10033	E70857	D70836	F70831	G70929	F70835	H70931	H70750	B70931	H70929	F70513	D70922	H70503	A70663	D70940	G70925	F70560	T45392	B70625	E70929	C70931	A70504	A70646	B87158	C70582	877655	B70932	E70675
	ength DB	368 2	302 2	434 2		518 2	393 2	536 2	403 2	463 2	423 2	350 2	473 2	391 2	385 2	391 2	556 2	408 2	413 2	572 2	391 2	365 2	463 2	394 2	380 2	468 2	423 2	438 2	468 2	406 2
Ouery	Match Length	99.3	27.9	22.8	22.8	21.4	20.3	20.2	20.1	19.9	19.9	19.8	19.7	19.6	19.5	19.3	19.3	19.1	•		18.6	18.6	18.4	18.2	18.2	•		17.2	17.1	17.0
	Score	1878	527	430.5	430.5	404.5	383.5	382	379.5	376.5	376	374	373	371	369.5	365.5	365	362	360.5	356	352	351.5	348	344.5	343.5	331	326	325.5	323.5	322.5
Result	No.		7	е	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	29

probable PPE prote probable PPE prote	probable PPE prote probable PPE prote	probable PPE prote probable PPE prote	hypothetical prote	Pre-ramily process probable PPE proce	probable PPE prote	probable FFB proce		probable PPE prote		probable PPE prote
G70881 A70932	B70608 A70899	A70882 H70741	C49930	C86976 C70780	C70568	D/05/5 H70857	A70647	F70675	G70570	A70931
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394	391	396	501	538 443	393	3300	409	582	580	655
16.9	16.8	16.6	16.5	16.0 15.8	15.8	15.3	15.2	15.2	14.6	14.4
319.5	315.5	315	311.5	303	299	289 288.5	287.5	287	276	272.5
30	3 7 8	3.4 4.7	36	37 38	39	4 4 1 4 1	42	43	44	45

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		probable PPE protein - Mycobacterium tuberculosis (strain	
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		PPE	C.Species: Mycobacterium tuberculosis
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RESULT	G70802	Spak	Spec
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S;Connor, R.; Davise, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Barrell, B.G.
A;Accession: G70802
A;Accession: G70802
A;Accession: G70802
A;Accession: G70802
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Modecule type: DNA
A;Residues: 1-368 <COL>
A;Residues: 1-368 <COL>
A;Residues: UNIPROT:069738; UNIPARC:UP10000165388; GB:AL022120; GB:AL123456; NI:
A;Gene: PPE

ö Gapa ô Length 368; Query Match
99.3%; Score 1878; DB 2; Length 3
Best Local Similarity 100.0%; Pred. No. 1.9e-104;
Matches 368; Conservative 0; Mismatches 0; Indels

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64 SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPBIAANHITQAVLT 123 124 ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPWASILDPGASQ 183 STINPI FGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG 243 184 셤 g ò Š ò 셤

GGNPADERAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLI 303 241 GGNPADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGGLTRTPLMSQLI 300 EKPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED 363 244 304 셤 g à ò

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A;Molecule type: DNA
A;Residues: 160-293, 'ASPFGGAVVGGVGRCCGSGCSWVGRGGGIGRSAGGGCGCWRAGG',338-354,' VGVGGAGSREH
A;Cross-referances: UNIPARC:UPI0000179FE0; EMBL:XS9271
A;Note: the authors identified this protein as dihydrofolate reductase
C;Genetics:
A;Gene: PPE
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A,Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 PGANEASNAVAAATITPFPWHEIVQFLEETFAAYDQYLSALLSELPAVAWVWFQLFVDIL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 -TQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVG---GTGGGGNPADBEAAQMGLLGTSPLS 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 NHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATGG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVLTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQABT-AVNTLFEKLEPMASILD
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 434;
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.8%; Score 430.5; DB 2; Best Local Similarity 33.2%; Pred. No. 1.5e-18; Matches 132; Conservative 45; Mismatches 158;
A;Reference number: S21832
A;Reference number: S21832
A;Accession: S21834
A;Molecult
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Best Local Similarity 33.33
Matches 134, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIDSTGVYTSAQRGDTESAHRIGLFGASTLSSHPLVGITGTTTDTRLLCAESLPSASGSL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SQ--STINPIFGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFS
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                                                   DWDEEDDW 368
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probable PPB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70229
R;Colle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Colle, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S. Raindream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-333 <COL>
A;Cross-references: UNIPROT:053939; UNIPARC:UPI00001652AA; GB:AL022021; GB:AL123456; NI:A;Experimental source: strain H37RV
C;Genetics:
A;Gene: PPB
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-010-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70835
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Esjandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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FDWPTHMLQLATWLAENPQLLVAALTPAISGLGAVSGLAGLTGLVPQPPVVPAPAPDAVV 335
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20.3%; Score 383.5; DB 2; Length :
Best Local Similarity 32.0%; Pred. No. 8.2e-16;
Matches 131; Conservative 38; Mismatches 156; Indels
                                                      PSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAP 350
                                                                                                    PTVLPLAGTATPTTAPASAPAAGA-APGPPAGTATATSASVP 376
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C; Date: 17.-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C; Accession: F7081
R; Devoin, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G., A; Ttele: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Accession: F70831
A; Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-518 <COL>
A; Residues: 1-518 <COL>
A; Cross-references: UNIPROT:O53738; UNIPARC:UPI0000004FC2; GB:AL021932; GB:AL123456; NIC
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                                                         120 AVLTAINFEGINTIPIALTEMDYFIRWMNQAALAMBVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                               121 TVLVATNPFGINTIPITLINBADY-VRMWLQAAAVMGLYQAASGAALASAPRTVPAPTVMN 179
                                                                                                                                                                                                                         224
                                                                                                                                                                                                                                                                                                                                                                                                                                       PLAGGSGPSAGAGL -- LRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATG 323
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                   TGGGSDKALAAATPWVWIQTASTQAKTRAWQATAQAAAYTQAMATTPSLPEIAANHITQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable PPB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                          180 PGGGAAST-----VGAVNPWQWILLALLQQLWNAYTGFYGWMLQLIWQFLQDPIGNSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 GAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDEDDW 365
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Cispecies: Mycobacterium tuberculosis

Cispecies: R; Brosers, J; Rutter, S; Feltwell, T; Churcher, C; Harris, D; Gordon, S; Connor, R; Davies, R; Devlin, K; Feltwell, T; Gantles, S; Hamilin, N; Holroyd, S. Nature 333, 537-544, 1998

Ajauchares: Sqares, J; Rutter, S; Seeger, K; Skelton, S; Squares, S. Natures; Sqares, R; Sulston, J.E.; Taylor, K.; Whitehead, S; Barrell, B.G.

Ajauchors: Sqares, R; Sulston, J.E.; Taylor, K.; Whitehead, S; Barrell, B.G.

Ajauchors: Sqares, R; Sulston, J.E.; Paylor, K.; Whitehead, S; Barrell, B.G.

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A,Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A,Reference number: A70500, MUID:98295987, PMID:9634230
A,Accession: F70835
A,Status: prelimary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-536 <COL>
A,Cross-references: UNIPARC:UPI00000D3AF4; GB:AL021930; GB:AL123456; NID:g3261524; PIDN: C,Genetics:
A,Gene: PPB
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                                                                                                                                                                                                                                                                                                                      tch 20.2%; Score 382; DB 2; Length 536; al Similarity 30.1%; Pred. No. 1.46-15; 134; Conservative 41; Mismatches 152; Indels 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 AQSGGSTRPGLVAPAPLAQEREEDD 361
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probable PPB protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-011-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: H70750

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davises, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998

A,Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A,Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70800; MUID:98295987; PMID:9634230

A,Accession: H70750

A,Estatus: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-463 <COL>
A,COLS-references: UNIPROT:Q10892; UNIPARC:UP1000013924F; GB:Z74410; GB:AL123456; NID:96
A,Experimental source: strain H37RV
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                                                                                                                         127
                                                                                                                                                                                         70 TAAAAPYVAWMSVTAVRAEQAGAQAEAAAAYEAAFAATVPPVIEANRAQLMALIATNV 129
                                                                                                                                                                                                                                                         ---- 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                 |: | | : | | : | | : | | 189 AIAHATGASAGAQQTTLSQLIAAIPSVLQGLSSSTAATFASGPSGLLGIVGSGSSWLDKL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :: :: :: :| |: | :|||| | #ALLIDPNSNFWNTIASSGLFLPSNTIAPFLGLLGGVAAADAAGDVLGEATSGGLGGALVA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TRLDVLSSIGQLIRDILDFIANPYKYFLEFFEQFGF-SPAVTVVLALVALQLYDFLWYPY 239
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MPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAWTGGGSDKA
                                        10 LPPEINSARMYSGAGSAPMLAAASAWHGLSAELRASALSYSSVLSTLTGEEWHGPASASM
                                                                                                                                                                                                                                                                                                                                                                                     ----ASILDPGASQSTTNP-IFGMPS--PG-SSTPVGQLPPAATQTLGQLGEMSGPMQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 PLGS---AGGLGGTVAAGLGNAATV----GTLSVPPSWT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 TQPLQQVTSLFSQVGGTGGGNPADEEAAQMGLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 30.39
Matches 119; Conservative
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-350 <COL>
A;Coss-references: UNIPROT:053940; UNIPARC:UPI00001652AB; GB:AL022021; GB:AL123456; NIIASCORDER: PPB
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Cibate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
CiAccession: F70513
RyCole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Brosch, R.; Devinn, K.; Feltwell, T.; Gentles, S.; Hamin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Ayauthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: F70513
A; Accession: F70513
A; Actus: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-473 <COLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 ALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQAVLTATN
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Pred. No. 4.2e-15;
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Best Local Similarity 32.9%; Pred. No. 2.6e-15;
Matches 124; Conservative 42; Mismatches 149
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28.9%;
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Best Local Similarity
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-011-1998 #sequence_revision 17-011-1998 #text_change 09-011-2004
C;Accession: 17-011-1998 #sequence_revision 17-011-1998 #text_change 09-011-2004
C;Accession: Broosth, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Broosth, R.; Parkhill, M.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70931
A;Accession: B70931
A;Residues: 1-423 <COL>
A;CL>
A;CLS
A;CLS
A;CRSS-references: UNIPROT:053950; UNIPARC:UPI00000D5E6B; GB:AL022021; GB:AL123456; NIE
A;Experimental source: strain H37RV
C;Genetics:
A;Genetics: PPB
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                               240 YASYGLILEPPFTFTLSALTALSALIHLINLPPAGLEPIAAALG-----PGDQWGANLA 293
                                                                                                                                                                                             257 LIGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAG--GSLTRTPLMSQLIEKPVAPSVMPA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable PPB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|| : : | |||| : | ||| | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTGPYTFPGVLPPSGVPYL--LGIQS---VLVTQNGQGVSALLGKIGGKPITGALAPLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 EAAOMGLIGTSPLSNHPLAGGSGPSAG---AGLIRAESLPGAGGSLTRTPLMSOLIEKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 MPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGGSDKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPPEINSGRMYTGPGPGPMLAAATAWDGLAVELHATAAGYASELSALTGAWSGPSSTSMA
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al Similarity 31.7%; Score 376; DB 2; Length 42
al Similarity 31.7%; Pred. No. 2.5e-15;
128; Conservative 35; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FALHTPILGSEGL-----GGGSVSAGIGRAGLVGKLSVPQGW----
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                                                                                                                                                                                                                                                                                                       315 AAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGL 347
                                                                                                                                                                                                                                                                                                                                                                          348 PKAGTKSPDTAADTLATA-----GAARPGL 372
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Best Local Similarity
Matches 128; Conserv
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0y 217	c;species: nycobaccerium constructs C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
### STATES CONSERVATIVE 42; Mismatches 117; Indels 94; Gaps 5 INTAMPERLYRANGARPHILAAARAGUTGALIANOAVELTARINSGRANTOGG 5 Hillie:	DD 185 GIQVAGMATTASAAVIEVVEGAMASVETVMSGMQSLVSQLEELGEASMLEEFVKIL 259

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C;Accession: A70663
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Decipharing the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MulD: 98295987; PMID: 9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Robecules type: DNA
A;Robecule type: DNA
A;Residues: 1-391 cCOL>
A;Cross-references: UNIPROT: P95247; UNIPARC: UPI00000D5E93; GB: Z83860; GB: AL123456; NID: GA; Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 LLRAESLPGAGGS--LTRTPLMSQLIEKPVAPSVMPAAAGSSATGGAA----- 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 -----MASILDPGASQSTTNPIFGMPS--PGSSTPVGQLPPAATQTLGQLGE-----MS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 GAQLICMAISVSAALSPIAEGAVEGVPAVVAAAOSVAAGLPVDAALQVGQAAAYPASMLI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 GPMMQLAQ-----MGTTANTAGLAGAEAAGLAAADV-----PTFAGDIASGTGLGGAGG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 LAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPBIAANHITQAVLTATNF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 AGAAAPYVGWISAAAGQAELSAGQATAAATAFBAALAATVHPAAVTANRVLLGALVATNI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 LGQNTPAIAATEFDY-VEMWAQDVGAMVGYHAGAA--AVAETLTPFSVPPLDLAGLASQA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 L-----GAGMSAELGKARLVGAMSVPPTWEGSVPARMASSAMAGLGAMPAEVPAAGGP 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 19.3%; Score 365.5; DB 2; Best Local Similarity 30.3%; Pred. No. 9.5e-15; Matches 120; Conservative 38; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- PVGAGAMGQGAQSG----GSTRPGLVAPAP 352
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Search completed: January 5, 2006, 21:15:37 Job time: 43 secs